

EXHIBIT 5

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

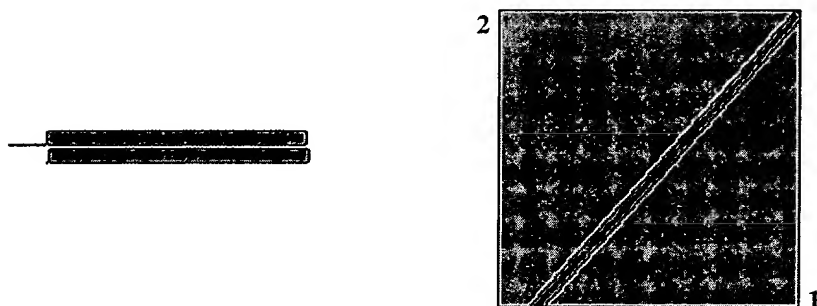
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☐ View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|1469860|dbj|BAA09787.1|leptin [Homo sapiens] >gi|4557715|ref|NP_000221.1| leptin precursor [Homo sapiens] >gi|730218|sp|P41159|LEP_HUMAN Leptin precursor (Obesity factor) (Obese protein) >gi|623332|gb|AAA60470.1| ob >gi|1226244|gb|AAC50400.1| obese protein >gi|1407583|dbj|BAA09839.1| ob protein [Homo sapiens] >gi|38174530|gb|AAH60830.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854318|gb|AAH69527.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854679|gb|AAH69452.1| Leptin (obesity homolog, mouse) [Homo sapiens]...
 Length = 167 (1 .. 167)

Sequence 2: gi|110666863|gb|ABG81864.1|obese protein [Anguilla japonica]
 Length = 146 (1 .. 146)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 241 bits (615), Expect = 1e-62
 Identities = 123/145 (84%), Positives = 136/145 (93%), Gaps = 0/145 (0%)

| | | | |
|-------|-----|---|-----|
| Query | 23 | PIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAVY | 82 |
| | | PIQKVQDDTKTLIKTIVTRINDISHTQSVS+KQ+VTGLDFIPGLHPIL+LSKMDQTLAVY | |
| Sbjct | 2 | PIQKVQDDTKTLIKTIVTRINDISHTQVSAKQRTGLDFIPGLHPILSLISKMDQTLAVY | 61 |
| Query | 83 | QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSKCHLPWASGLETLDLGGVLEASGYST | 142 |
| | | QQ+LTS+PS+NV+QI+NDLENLRDLLH+LAFSKSC LP SGL+ +SL GVLEAS YST | |
| Sbjct | 62 | QQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLPQTSGLQKPESLDGVLEASLYST | 121 |
| Query | 143 | EVVALSRLQGSLQDMLWQLDLSPGC | 167 |
| | | EVVALSRLQGSLQD+L QLD+SP C | |
| Sbjct | 122 | EVVALSRLQGSLQDILQQLDVSPEC | 146 |

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

| Lambda | K | H |
|--------|-------|-------|
| 0.321 | 0.135 | 0.415 |

Gapped

| Lambda | K | H |
|--------|--------|-------|
| 0.267 | 0.0410 | 0.140 |

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 262

Number of extensions: 97

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 167

Length of database: 1,565,033,500

Length adjustment: 124

Effective length of query: 43

Effective length of database: 1,565,033,376

Effective search space: 67296435168

Effective search space used: 67296435168

Neighboring words threshold: 9

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 73 (32.7 bits)